



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/922,067 D  
Source: 1600  
Date Processed by STIC: 10/2/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/cbc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service; Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mallroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

09/922,067D

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length     Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
                    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    This sequence is intentionally skipped  
  
                    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
                    <210> sequence id number  
                    <400> sequence id number  
                    000
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.
- 11 ✓ Use of <220>     Sequence(s) 5-7 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa     "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/922,067D

DATE: 10/02/2003

TIME: 15:54:11

Input Set : A:\p30693c4x1c1seqlist.txt

Output Set: N:\CRF4\10022003\I922067D.raw

4 <110> APPLICANT: MacPhee, Colin Houston  
 5     Tew, David Graham  
 6     Southan, Christopher Donald  
 7     Hickey, Deirdre Mary Bernadette  
 8     Gloger, Israel Simon  
 9     Lawrence, Geoffrey Mark Prouse  
 10    Rice, Simon Quentyn John  
 12 <120> TITLE OF INVENTION: Lipoprotein Associated Phospholipase A2,  
 13     Inhibitors Thereof and Use of the Same in Diagnosis and  
 14     Therapy  
 16 <130> FILE REFERENCE: F30693C4X1C1  
 18 <140> CURRENT APPLICATION NUMBER: 09/922,067D  
 19 <141> CURRENT FILING DATE: 2001-08-03  
 21 <150> PRIOR APPLICATION NUMBER: 09/193,130  
 22 <151> PRIOR FILING DATE: 2000-11-28  
 24 <150> PRIOR APPLICATION NUMBER: 08/387,858  
 25 <151> PRIOR FILING DATE: 1994-06-24  
 27 <150> PRIOR APPLICATION NUMBER: PCT/GB94/01374  
 28 <151> PRIOR FILING DATE: 1994-06-24  
 30 <150> PRIOR APPLICATION NUMBER: GB 9313144.9  
 31 <151> PRIOR FILING DATE: 1993-06-25  
 E--> 33 <160> NUMBER OF SEQ ID NOS: (11) 13 (see below)  
 35 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Does Not Comply  
Corrected Diskette Needed

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## ERRORED SEQUENCES

309 <210> SEQ ID NO: 12  
 310 <211> LENGTH: 7  
 311 <212> TYPE: PRT  
 312 <213> ORGANISM: Homo sapien  
 E--> 314 <400> SEQUENCE: (10) 125 Large to  
 315 Gln Tyr Ile Asn Pro Ala Val  
 316 1 5  
 319 <210> SEQ ID NO: 13 last sequence in submitted file  
 320 <211> LENGTH: 5  
 321 <212> TYPE: PRT  
 322 <213> ORGANISM: Homo sapien  
 E--> 324 <400> SEQUENCE: (10) 13  
 325 Gln Tyr Ile Asn Pro  
 326 1 5  
 330 6/6 delete

09/922,0670 Z

<210> 5  
<211> 420  
<212> DNA  
<213> Unknown

*needs explanation (see item 11 on Error Summary Sheet)*

<220>  
<221> misc\_feature  
<222> 265, 390, 395, 403, 406  
<223> n = A,T,C or G

<400> 5  
aaaaaaccta ttttaatcct aattgtattt ctctattcct gaagagttct gtaacatgat 60  
gtgttgattg gttgtgttaa tgttggtccc tggaataaga ttctcatcat ctcttcaat 120  
caagcagtc cactgatcaa aatctttatg aagtcctaaa tgcttttgta agaattgctaa 180  
tgaagctttg ttgctaagat caatagctgc atttgaatct atgtctccct ttaatttgag 240  
catgtgtcca attattttgc cagtngcaaa agtgaagtca gcaaaattct ggtggactga 300  
accctgatt gtaatcatct ttctttcttt atcaggtgag tagcattttt tcatttttat 360  
gatattagca ggatattgga aatattcagn gttgntaaaa agngngggct gagggattct 420

<210> 6  
<211> 379  
<212> DNA  
<213> Unknown

*same error*

<220>  
<221> misc\_feature  
<222> 84  
<223> n = A,T,C or G

<400> 6  
tgctaataatc ataaaaatga aaaaatgcta ctcacctgat aaagaaagaa agatgattac 60  
aatcaggggt tcagtcacac aganttttgc tgacttcaact ttgcaactg gcaaaataat 120  
tggacacatg ctcaaattaa agggagacat agattcaaatt gtagctattg atcttagcaa 180  
caaagcttca tttagcattct taaaaagca tttaggactt cataaagatt ttgttcagtg 240  
ggactgcttg attgaaggag atgatgagaa tcttattcca gggaccaaca ttaacacaac 300  
caattcaaca catcatgttt acagaacttc ttccaggga taggaggaaa tacaattggg 360  
gtttaaaata ggttttttt 379

<210> 7  
<211> 279  
<212> DNA  
<213> Unknown

*same*

<220>  
<221> misc\_feature  
<222> 257  
<223> n = A,T,C or G

<400> 7  
gaagaatgca tttagatttaa agtttgatat ggaacaactg aaggactcta ttgataggga 60  
aaaaatagca gtaattggac attcttttgg tggagcaacg gttattcaga ctcttagtga 120  
agatcagaga ttcagatgtg gtattgcctt ggatgcatgg atgtttccac tgggtgatga 180  
agtatatcc agaattcttc agccctctt ttttatcaac tctgaatatt tccaatatcc 240  
tgctaataatc ataaaantgg aaaaatgcta ctcacctgg 279

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/922,067D

DATE: 10/02/2003

TIME: 15:54:12

Input Set : A:\p30693c4x1c1seqlist.txt

Output Set: N:\CRF4\10022003\I922067D.raw

L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:240  
M:341 Repeated in SeqNo=5  
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:60  
L:141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:240  
L:314 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:12 differs:10  
L:324 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:13 differs:10  
L:33 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (11) Counted (13)